



04-29-02

GP/1646

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
(Case No. 00-1213)

PATENT

In re Application of: Saris et al.
Serial No.: 09/724,583
Filed: November 28, 2000
For: Interleukin-1 Receptor
Antagonist-Related Molecules
and Uses Thereof

Before the Examiner: P. M. Mertz
Group Art Unit: 1646

Commissioner for Patents
Washington, D.C. 20231

Sir:

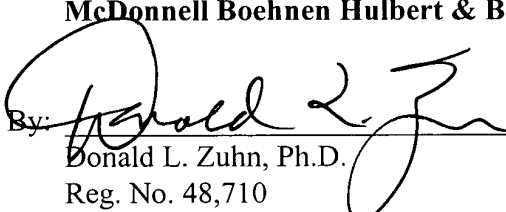
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TRANSMITTAL LETTER

1. We are transmitting herewith the attached papers for the above-described patent application:
Response to Restriction Requirement.
2. GENERAL AUTHORIZATION TO CHARGE OR CREDIT FEES: Please charge any additional fees or credit any overpayment to Deposit Account No. 13-2490.
3. CERTIFICATE OF MAILING BY "EXPRESS MAIL" UNDER 37 C.F.R. 1.10: The undersigned hereby certifies that this Transmittal Letter and the papers, as described in paragraph 1 hereinabove, are being deposited with the United States Postal Service with sufficient postage as "Express Mail Post Office to Addressee" in an envelope addressed to: Commissioner for Patents, Washington D.C. 20231, on April 26, 2002.

Respectfully submitted,
McDonnell Boenken Hulbert & Berghoff

Dated: April 26, 2002

By: 
Donald L. Zuhn, Ph.D.
Reg. No. 48,710



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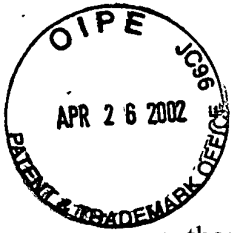
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Washington, D.C. 20231

Sir:

RESPONSE TO RESTRICTION REQUIREMENT MAILED MARCH 26, 2002

Responsive to the Restriction Requirement, mailed March 26, 2002, Applicants elect to prosecute claims 1-8, 10, 11, and 42-46, designated as Group II by the Examiner, with traverse. The claims of Group II are drawn to a polynucleotide encoding an IL-1 receptor antagonist-like polypeptide as set forth in SEQ ID NO: 2, a vector, a host cell, and a process for producing the polypeptide. The basis for Applicants' traversal of the requirement is as follows.

Applicants respectfully submit that there will be no undue hardship on the Office in performing a search with respect to polynucleotides encoding the IL-1 receptor antagonist-like polypeptides set forth in SEQ ID NOs: 2, 4, and 6. The IL-1 receptor antagonist-like polypeptides set forth in SEQ ID NOs: 2 and 4, both of which are 152 amino acids in length, share a sequence identity of 98% (Exhibit A). The IL-1 receptor antagonist-like polypeptide set forth in SEQ ID NO: 6, which is 171 amino acids in length, shares a sequence identity of at least 87% with the IL-1 receptor antagonist-like polypeptides set forth in SEQ ID NOs: 2 (Exhibit B) and 4 (Exhibit C). Moreover, the IL-1 receptor antagonist-like polypeptide set forth in SEQ ID NO: 6 shares a sequence identity of at least 98% with the IL-1 receptor antagonist-like polypeptides set forth in SEQ ID NOs: 2 and 4 when only residues 20 through 171 of SEQ ID NO: 6 are considered. Sequence alignments were performed using the application MacVector 7.1.1 (Accelrys, Cambridge, UK; <http://www.accelrys.com>) at the default settings.



Applicants do not believe that any additional fee is required. However, the Commissioner is authorized to charge any deficiency to Deposit Account No. 13-2490. If Examiner Mertz believes it to be helpful, she is invited to contact the undersigned representative by telephone at (312) 913-0001.

Respectfully submitted,
McDonnell Boennen Hulbert & Berghoff

Dated: April 26, 2002

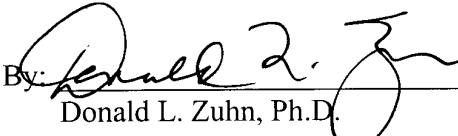
By: 
Donald L. Zuhn, Ph.D.
Reg. No. 48,710



EXHIBIT A

Aligned Length = 152 Gaps = 0
Identities = 150 (98%) Similarities = 0 (0%)

```
SEQ02    1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEEKICTLPNRGL   50
SEQ04    1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEEKICILPNRGL   50
          *****

SEQ02    51 DRTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEETRFT  100
SEQ04    51 ARTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEETRFT  100
          *****

SEQ02   101 FFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFEQ  150
SEQ04   101 FFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFEQ  150
          *****

SEQ02   151 SW 152
SEQ04   151 SW 152
          **
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EXHIBIT B

Aligned Length = 171 Gaps = 0
Identities = 150 (87%) Similarities = 0 (0%)

```
SEQ06   1  MVLSGALCFREDQTPLIAGMCSLPMARYYIIKYADQKALYTRDGQLLVGD   50
SEQ02   1                                MCSLPMARYYIIKYADQKALYTRDGQLLVGD   31
                                     *****

SEQ06   51  PVADNCCAEEKICILPNRGLARTKVPIFLGIQGGSRCLACVETEEGPSLQL  100
SEQ02   32  PVADNCCAEEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEGPSLQL   81
                                     *****

SEQ06  101  EDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQP  150
SEQ02   82  EDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQP  131
                                     *****

SEQ06  151  VQLTKESEPSARTKFYFEQSW  171
SEQ02  132  VQLTKESEPSARTKFYFEQSW  152
                                     *****
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EXHIBIT C

Aligned Length = 171 Gaps = 0
Identities = 152 (88%) Similarities = 0 (0%)

```
SEQ06    1  MVLSGALCFREDQTPLIAGMCSLPMARYYIIKYADQKALYTRDGQLLVGD  50
SEQ04    1                                MCSLPMARYYIIKYADQKALYTRDGQLLVGD  31
                                     *****

SEQ06    51  PVADNCCAEEKICILPNRGLARTKVPIFLGIQGGSRCLACVETEEGPSLQL 100
SEQ04    32  PVADNCCAEEKICILPNRGLARTKVPIFLGIQGGSRCLACVETEEGPSLQL  81
                                     *****

SEQ06   101  EDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQP 150
SEQ04    82  EDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQP 131
                                     *****

SEQ06   151  VQLTKESEPSARTKFYFEQSW 171
SEQ04   132  VQLTKESEPSARTKFYFEQSW 152
                                     *****
```